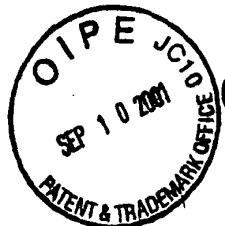


REPORTS - 000000



SEQUENCE LISTING

<110> DYAX Corp.
Ley, Arthur C.
Luneau, Christopher J.
Ladner, Robert C

<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

<130> DYX-012.1 US, DYX-012.1 PCT

<140> 09/884,767
<141> 2001-06-19

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<151> 2000-06-19

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Xaa Xaa Xaa Xaa Xaa Xaa Gly Ala Gln Ser Asp Gly Gly Ser
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09897257-091004

TOOTSOO-AEDHSS60

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DRAFT - DO NOT CITE

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Tyr Ala Gln Asp Glu Arg Thr
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TOOT60" X92418860

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Gly Gly Arg Glu Glu Arg Asn
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Gly Ser Gly Gly Asp Arg Met
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Ile Ala Tyr Gln Asp Arg Met
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Ser Leu Asp Asp Asp Arg Thr
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Ser Gly Gly Gln Glu Arg Ser
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TOP SECRET//COMINT

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Gly Ser Gly Gly Asp Arg Ile
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TOOTED" 9/27/860

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Gly Phe Val Gln Glu Arg Met
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Asp Ile Asn Asp Asp Arg Ser
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Ala Ala Val Glu Asp Arg Asn
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Asp Tyr Arg Leu Asp Arg Ile
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Gly Asp Asp Asp Asp Lys Ile
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Ala Val Leu Ser Asn Val Met His Ser Asp Asp Trp Thr
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Gly Asp Asp Asp Asp Lys Ile Tyr Val
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<223> negative control in EK cleavage experiment

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Ala Val Leu Ser Asn Val Met Phe Ile
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Gly Asn Tyr Thr Asp Arg Met Phe Ile
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Asn Lys Ala Lys Asp Arg Met Phe Ile
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Gly Asn Tyr Thr Asp Arg Arg Phe Ile
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<223> commercial synthetic enterokinase cleavage substrate

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Gly Asn Tyr Thr Asp Arg Tyr Phe Ile
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<210> 204

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<223> synthetic enterokinase cleavage sequence

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<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is any amino acid

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Asp Ile Asn Asp Asp Arg Xaa
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<223> synthetic enterokinase cleavage sequence

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<222> (7)..(7)

<223> Xaa is any amino acid

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1 5

<210> 206

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic enterokinase cleavage sequence

<220>

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□□□□□□□□□□□□□□□□□□

<222> (1)..(1)
<223> Xaal is an optional amino acid which, if present, is Ala, Asp, Glu, Phe, Gly, Ile, Asn, Ser, or Val

<220>
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<222> (2)..(2)
<223> Xaa2 is an optional amino acid which, if present, is Ala, Asp, Glu, His, Ile, Leu, Met, Gln, or Ser

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa3 is an optional amino acid which, if present, is Asp, Glu, Phe, His, Ile, Met, Asn, Pro, Val, or Trp

<220>
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<222> (4)..(4)
<223> Xaa4 is Ala, Asp, Glu, or Thr

<220>
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<222> (7)..(7)
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<400> 206

Xaa Xaa Xaa Xaa Asp Arg Xaa
1 5

<210> 207
<211> 7
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<220>
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<223> Xaal is an optional amino acid which, if present, is Asp or Glu

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa2 is an optional amino acid which, if present, is Val

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<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa3 is an optional amino acid which, if present, is Tyr
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<220>
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<222> (4)..(4)
<223> Xaa4 is Asp, Glu or Ser
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<223> Xaa7 is any amino acid
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Xaa Xaa Xaa Xaa Glu Arg Xaa
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<400> 208

Asp Ile Asn Asp Asp Arg
1 5

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<400> 209

Gly Asn Tyr Thr Asp Arg
1 5

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Trp His Pro Gln Phe Ser Ser
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Pro Cys His Pro Gln Phe Pro Arg Cys Tyr
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<400> 212

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gacgacaaaaa ctttagatcg ttacgctaacc tatgagggtt gtctgtggaa tgctacaggc 180

gtttagttt gtactggtga cgaaaactcag tgttacggta catgggttcc tattgggctt 240

gctatccctg aaaatgaggg tggtggctct gagggtggcg gttctgaggg tggcggttct 300

gagggtggcg gtactaaacc tcctgagttac ggtgatacac ctattccggg ctataacttat 360

atcaaccctc tcgacggcac ttatccgcctt ggtactgagc aaaaccccgc taatccataat 420

ccttctcttg aggagtctca gcctcttaat actttcatgt ttcagaataa taggttccga 480

aataggcagg gggcattaac tggttatacg ggcactgtta ctcaaggcac tgaccccggtt 540

aaaacttattt accagtacac tcctgtatca tcaaaagcca tgtatgacgc ttactggaac 600

ggtaaattca gagactgcgc tttccattct ggctttaatg aagatccattt cgtttgcgaa 660

tatcaaggcc aatcgctctga cctgcctcaa cctcctgtca atgctggcggttgcg 720

ggtggttctg gtggcggttc tgagggtgggttgcg ggcgtctgagg gtggcggttc tgagggtggc 780

DRAFT 5.0 X924748650

ggctctgagg gaggcggttc cggtggtggc tctggttccg gtgattttga ttatgaaaag	840
atggcaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc gctacagtct	900
gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat cgatggtttc	960
attggtgacg tttccggcct tgctaatttgt aatggtgcta ctggtgattt tgctggctct	1020
aattcccaaa tggctcaagt cggtgacggt gataattcac cttaatgaa taattccgt	1080
caatatttac ctccccccc tcaatcggtt gaatgtcgcc cttttgtctt tagcgctggt	1140
aaaccatatg aattttctat tgattgtgac aaaataaact tattccgtgg tgtctttgcg	1200
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Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser			
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His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu		
20	25	30

Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr		
35	40	45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys		
50	55	60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu			
65	70	75	80

Ala Ile Pro Glu Asn Glu Gly Gly Ser Glu Gly Gly Ser Glu		
85	90	95

Gly Gly Gly Ser Glu Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp		
100	105	110

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr
115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu
130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg
145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly
165 170 175

Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys
180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe
195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln
210 215 220

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Ser Gly
225 230 235 240

Gly Gly Ser Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Gly
245 250 255

Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly
260 265 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
275 280 285

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
290 295 300

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
305 310 315 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
325 330 335

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Phe Ala Gly S r Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
340 345 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
355 360 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
370 375 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
385 390 395 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
405 410 415

Asn Ile Leu Arg Asn Lys Glu Ser
420

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tctcagcctc ttaataacttt catgtttcag aataataggt tccgaaatag gcagggggca 180

ttaactgttt atacgggcac tgttactcaa ggcactgacc ccgtaaaac ttattaccag 240

tacactcctg tatcatcaaa agccatgtat gacgcttaact ggaacggtaa attcagagac 300

tgcgcttcc attctggctt taatgaagat ccattcgaaa gtgaatatacg aggccaatcg 360

tctgacctgc ctcaacctcc tgtcaatgtt ggccggcgct ctgggtgggg ttctggggc 420

ggctctgagg gtgggtggc tgagggtggc ggttctgagg gtggcggtc tgaggaggc 480

ggttccggtg gtggctctgg ttccggtgat tttgattatg aaaagatggc aaacgctaat 540

aagggggcta tgaccgaaaa tgccgatgaa aacgcgtac agtctgacgc taaaggcaaa 600

cttgattctg tcgctactga ttacggtgat gctatcgatg gtttcattgg tgacgtttcc 660

ggccttgcta atggtaatgg tgctactggat gatggctg gctctaattc ccaaattggct 720

caagtcggtg acggataa ttcaccttta atgaataatt tccgtcaata tttaccttcc 780
ctccctcaat cggttgaatg tcgcctttt gtcttagcg ctggtaaacc atatgaattt 840
tctattgatt gtgacaaaat aaacttattc cgtggtgtct ttgcgtttct tttatatgtt 900
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<400> 215

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Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala
20 25 30

Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met
35 40 45

Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr
50 55 60

Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln
65 70 75 80

Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly
85 90 95

Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe
100 105 110

Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
115 120 125

Asn Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly
130 135 140

Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly
145 150 155 160

Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met
165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala
180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr
195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn
210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala
225 230 235 240

Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln
245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe
260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn
275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met
290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
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<400> 216

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gctgctatcg atggttcat tggtgacgtt tccggccttg ctaatggtaa tggtgctact 180

ggtgattttg ctggctctaa ttcccaaatg gctcaagtcg gtgacggta taattcacct 240
ttaatgaata atttccgtca atatttacct tccctccctc aatcggttga atgtcgccct 300
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Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu
20 25 30

Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly
35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asn Ser Pro
65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val
85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser
100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu
115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile
130 135 140

Leu Arg Asn Lys Glu Ser
145 150

100 150 200 400 800 0

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<211> 7
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<400> 122

Ser Gly Gly Glu Asp Arg Ala
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Leu Glu His Ser Asp Arg Val
1 5

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Phe Lys Pro Asp Asp Arg Met
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Val Pro Met Ala Asp Arg Ser
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Gly Ser Gly Gly Glu Arg Ala
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Asn Asp Asn Asp Glu Arg Ala
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Gly Asn Tyr Thr Asp Arg Met
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Gly Ser Gly Gly Glu Arg Val
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DRAFT = DRAFT

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Asp Glu Val His Asp Arg Thr
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Gln His Asp Gly Asp Lys Thr
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